

Untitled-12 Formatted Alignment

HTLV-III: HIV-I
Env Alignment

HTLV-II Env	M-----GNVF--FLI-----LFS-----	11
HTLV-I Env	-----GKFLATLIL-----FFQ-----	13
HIV SF2 Env	MTARGTRKNYQRLWRWGIML LGMLMICSAA ENLWVTVYVG VPVWKEATTT	50
Consensus	M-----G..L...LI-----F.-----	50

HTLV-II Env	-LT--HFPLAQ--QS-----FC-----TLTIC--IS--SY-----	32
HTLV-I Env	-FC--PLIFGDYSP-----C-----TLTIC--VS--SY-----	36
HIV SF2 Env	LFCASDARAYATEVHNWVAT HAOVPTDPNP QEVVLGNVTE NFDMWKNNMV	100
Consensus	-FC-----A....S-----C-----TLTIC--S--SY-----	100

HTLV-II Env	-----SS-SPGSPTQPM-----	45
HTLV-I Env	-----SS-KPQNPACPM-----	49
HIV SF2 Env	EQMQEDIISLWDGSLKPOVKLTPLQVTLDC TDVNTTSSSL RNATNTTSSS	150
Consensus	-----SS-KPQ.P.QEPM-----S-----	150

HTLV-II Env	-----NEELNSLT TDC--RL--H-----	60
HTLV-I Env	-----TEELLALSADQ--AL--Q-----	64
HIV SF2 Env	WEIMEKGELKNCSFNITTSIRDKMQEQYAL FYKLDVLPID KNETKFRLLH	200
Consensus	-----LELL.L..DQ--RL--H-----	200

HTLV-II Env	-----PFCENL-----I TY--SGF-----HKTYS-----	77
HTLV-I Env	-----PFCENL-----V SY--SSY-----HATYS-----	81
HIV SF2 Env	CNISTITQACPKISFEPIPM HYCTPAGFAI LKCNDKKFNG TGPCTNVSTV	250
Consensus	-----PFCENL-----M--SGF-----HKTYS-----	250

HTLV-II Env	-----EYME-----F-----	81
HTLV-I Env	-----EYME-----F-----	85
HIV SF2 Env	QCTHGIKPVVSTQILLNGSL AEEVEVIIRSS NFINNAKIII VQLNKSVEIN	300
Consensus	-----EYME-----F-----	300

HTLV-II Env	-----EYME-----F-----	86
HTLV-I Env	-----EYME-----F-----	90
HIV SF2 Env	CTRENNNTRNRISIGPGRAF HTTKQIIGDI RQAHCNLSRA TWKITLEQIA	350
Consensus	-----EYME-----F-----	350

HTLV-II Env	-----KPNR-----GLGYSSFSYNDE-----GS--LQCP-----Y-----	110
HTLV-I Env	-----KPNR-----GGGYSSAAYSDE-----GS--LKCP-----Y-----	114
HIV SF2 Env	TKLRKQFFNK TIAFDRSSGG DEEIVMHSFN GGGEFFYENT SQLFNSTWND	400
Consensus	-----KPNR-----G.GYSS.SY.DE-----GS--L.QP-----Y-----	400

HTLV-II Env	-----EYME-----F-----TSAYTGPFSS-----	126
HTLV-I Env	-----EYME-----F-----TCFYTGAASS-----	130
HIV SF2 Env	TTRANSTEVTTLEPRIKQIVMMDQEVGKAMYAPPISGQIRCSSKITGLL	450
Consensus	-----EYME-----F-----T..MDGPASS-----	450

Untitled-12 Formatted Alignment

HTLV-II Env	-----P-----SA-----KF-----	131
HTLV-I Env	-----P-----YA-----KF-----	135
HIV SF2 Env	LTRDGGKNTT NGIEIFRPAG GDMRDNMRSE LMKYKVVKIE PLGVAPTAR	500
Consensus	-----P-----A-----KF-----	500
HTLV-II Env	-----HSD-----VN-----E-----	137
HTLV-I Env	-----QHD-----VN-----E-----	141
HIV SF2 Env	RRVVOREKRA VGMLGAMFLG FLGAAGSTMG ARSMTLTVQA RQLLSGIVQQ	550
Consensus	-----Q.D-----VN-----E-----	550
HTLV-II Env	-----TQ-----VSQVSLRL-----HFSK-----CGSS	156
HTLV-I Env	-----TQ-----VSRLNINL-----HFSK-----CGFP	160
HIV SF2 Env	QNNLLRAIEA QHLLQLTVW GIKQLQARVL AVERYLKDOQ LLGIWGC SGK	600
Consensus	-----TQ-----VSQ...RL-----HFSK-----CG..	600
HTLV-II Env	M-----P-----E-----EYEA-----	163
HTLV-I Env	F-----P-----E-----EYEA-----	167
HIV SF2 Env	LICTTTVPWN ASWSNKSINE IWDNMTWMQW EREIDNYTHL IYTLIESQN	650
Consensus	.-----P-----E-----EYEA-----	650
HTLV-II Env	-----P-----YDP---LAF ITSEPTQPPP TSPPLVHSD	191
HTLV-I Env	-----P-----YDP---LAF LNTEPSQLPP TAPPLLPHSN	195
HIV SF2 Env	QQEKNEQELL ELDKWAGLWS WFSITNWLAY I-----	681
Consensus	-----P-----YDP---LAF I..EP.Q.PP T.PPL...S.	700
HTLV-II Env	LEHVLTPSTS WTKILKFYQ LTLQSTNYSC MCVDRSSLS SWHLYIPNI	241
HTLV-I Env	LDHILEPSIP WSKLLTLAQ LTLQSTNYTC IVCIDRASLS TWHLYSPNV	245
HIV SF2 Env	-----RI---F-----II---GGIV GLRIVFAV-L	701
Consensus	L.H.L.PS.. W..KIL.FYQ LTLQSTNY.C IVCIDR.SLS .WHLYIPN.	750
HTLV-II Env	STPQQTSSRT ILFPSALPA PP-SQFPFWT HCYCPRLQAI TTDNCNNSII	290
HTLV-I Env	SYP-SSSSTP LLYPSALPA PHLTLPFNWT HCFPQIQAI VSSPCHNSLI	294
HIV SF2 Env	ST---VNRVR QGYSELS-----FQTR-----	719
Consensus	STP-...SS.. .LYPSALPA P-...PF.WT HCFQPR.QAIC.NS.I	800
HTLV-II Env	GPFFSLAPVP PPATRRRRAV PIAVWLVSAL AAGTGIAGGV TGSLSLASSK	340
HTLV-I Env	GPFFSLSPVP TLGSRSRRAV PVAVWLVSAL AMGAGVAGGV TGSMASLASGK	344
HIV SF2 Env	LP-----TQR-----CPDRPEGIEEE-----	735
Consensus	GPFFSL.PVPR.RRAV P.AVWLVSAL A.G.G.AGGT TGS.SLAS.K	850
HTLV-II Env	SLLEVEKRII SHLTQAIVKNIHQNIIRVAQY AAQNRRGIDL LFWEGGGICK	390
HTLV-I Env	SLLEVEKRII SOLTQAIVKNIHKNIIRVAQY AAQNRRGIDL LFWEGGGICK	394
HIV SF2 Env	---GGFR---RDRSGRIVDGF-----LA---LWDT---LR	760
Consensus	SLL.EVDEKRII S.LTQAIVKNIH.N.I.RVAQY AAQNRRGIDL LFWEGGGICK	900

Untitled-12 Formatted Alignment

HTLV-II Env	AIQECCFLN	ISNTHVSILQ	ERPHEKRV	ITGWGLNDELG	LSQAREALQ	440
HTLV-I Env	ALQECCRFNP	ITNSHVPIIQ	ERPHEENRVL	ITGWGLNDELG	LSQAREALQ	444
HIV SF2 Env	SL-CLFSYHR	LRDLILIVAR	IVELLGRGW	EVLKYWNL	IQYWSQLKN	808
Consensus	ALQECC.F.N	I.N.HV.VLQ	ERPHE.EV.	ITGWGLNDELG	LSQAREALQ	950

HTLV-II Env	IGTHILALLL	LVILFGPCIL	ROIQALPQR	LQNRHNQYSL	INPEIM	486
HTLV-I Env	IGTHILVALLL	LVILAGPCIL	ROLRHLPQR	VRYPHYSL--	IKPEST	488
HIV SF2 Env	SVISLLNATA	IAVAEGTDRV	IEIVQRAYRA	FLNIPRRIRQ	GLERALT	855
Consensus	IGTHILALLL	LVIL.GPCIL	ROI..LP.R	..N.H.....	I.PE..	997

HTLV-I/II Env
ALIGNMENT

HTLV-II Env	MCNVF--FLLESLTHFPLA Q--QS	46
HTLV-I Env	MCKFLATLILFFQFCPLIFG DYSP	50
Consensus	MC.....L..E.....S	50
HTLV-II Env	NLDINSLTIDQRTHPPCPNLITYS	96
HTLV-I Env	TLDLIALSADQALPPCPNLVSY	100
Consensus	LDL..L..D..L..PPCPNL..VS	100
HTLV-II Env	SESNDPCSLCPVYLGCOAWTS	146
HTLV-I Env	SASNDPCSLKCPVYLGCOAWT	150
Consensus	S..SV..DPCSL..CPVYLGCO..W..T	150
HTLV-II Env	RLHFSKCGSSMTLLVDAPGYDE	196
HTLV-I Env	NLHFSKCGFPFSLIVDAPGYDP	200
Consensus	..LHFSKCG..MTLLVDAPGYDE	200
HTLV-II Env	TPSTSMITKILKFTQLTLQS	246
HTLV-I Env	EPSIPAKSKLITLQLTLQS	249
Consensus	..ES..M..K..L..KFTQLTLQS	250
HTLV-II Env	TSSRTILFPSLALPAPP-SQ	295
HTLV-I Env	SSSTPLIMPSLALPAPHLTL	299
Consensus	..SS...L..PSLALPAD....	300
HTLV-II Env	LPPVEPPATRERRAVEIAVW	345
HTLV-I Env	LPPVETLGSRERRAVEIAVW	349
Consensus	..L..VE...R..ERRAVEIAVW	350
HTLV-II Env	VEKDIESHETQAEVKNECNIL	395
HTLV-I Env	VEKDIESHETQAEVKNECNIL	399
Consensus	VEKDIESHETQAEVKNECNIL	400
HTLV-II Env	GOELNLSNTHVSLQERDPEL	445
HTLV-I Env	QRTFNHNSVPLQERDPEL	449
Consensus	..L..N..L..N..V..LQERDPEL	450
HTLV-II Env	LAIHHVNIFFEPQIERCIQA	486
HTLV-I Env	VAHHVNIFFEPQIERCLRH	488
Consensus	..LAIHHVNIFFEPQIERC...Q	491

HILW-II R01 Alignment

- 1 -

Untitled-14 Formatted Alignment

HTLV-II Pol	HTLV-I Pol	Consensus	600
HTLV-II Pol	HTLV-I Pol	Consensus	650
HTLV-II Pol	HTLV-I Pol	Consensus	700
HTLV-II Pol	HTLV-I Pol	Consensus	750
HTLV-II Pol	HTLV-I Pol	Consensus	800
HTLV-II Pol	HTLV-I Pol	Consensus	850
HTLV-II Pol	HTLV-I Pol	Consensus	900
HTLV-II Pol	HTLV-I Pol	Consensus	949
HTLV-II Pol	HTLV-I Pol	Consensus	982

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HTLV-I/II: HIV-1
Pol Alignment

HTLV-II Pol	HRSRPYGYTP -DTRARAGKA PRHPDPR---	RCWANQH--	PVQTPPNPPT	43
HTLV-I Pol	GKKAACNLA- -----	--NTGAS--	REWA-----	21
HIV SF2 Pol	FFREDLAFPQ GKAREFSSEQ TRANSPTSRE	LRVWGRDNNS	PSEAGADRQG	50
Consensus-..-..R.....R...P---	ELWA.....	P...TP.....	50
HTLV-II Pol	HI-LALRKVP -RYPFLPLR HPQOMDH---	-----	-----HWKG	72
HTLV-I Pol	-----RKAP -R-----	-----	-----	26
HIV SF2 Pol	TVSFNLQIT LWQRPIVTIK IGGQLKEALL	DTGADDTVLE	EMNLPGRWKP	100
ConsensusLEK.P -R.....Q....	-----	-----WK.	100
HTLV-II Pol	RPTTMPGASI PPRR-----	-----	-----PQPPPI	102
HTLV-I Pol	-----	-----	-----	26
HIV SF2 Pol	KMIGGIGGFI KVRQYDQILI EICGHKAIGT	VLVGPTFVNI	IGRNLLTQLG	150
ConsensusG..I ..R-----	-----	-----P.P..I	150
HTLV-II Pol	PRTSPSTSP- -SGEISFKKE ----RLQ--A	END-----	LV S--KAIE-AG	136
HTLV-I Pol	-----NQIPPFKKE ----RLQ--A	LOH-----	LV R--KAIE-AG	51
HIV SF2 Pol	CTLNFPISPI ETVEKIKKPG MDGPKVKQWP	ITEEKIKVLI	EICTEMEKEG	200
ConsensusP.SP- --..EV.FKKE ----RLQ--A	U...-----	LV...-KAIE-AG	200
HTLV-II Pol	HIEPYS--GE GNEVEPKK PNG-KWRFIH	ELRATNALT	TLTSPSPGGE	183
HTLV-I Pol	HIEPYT--GE GNEVEPKK ANG-TWRFIH	ELRATNALT	DLSSSSPGGE	98
HIV SF2 Pol	KISKVGPENP YNIPVEAIKK KESTKWKLV	DFRELKRIQ	DFWEVQLGIP	250
Consensus	HIEPY.--GE GNEVEPKK .NG-KWRFIH	ELRATN...I.	DL.S.SPGE	250
HTLV-II Pol	DLISPTALP HLQTIIDTDA FEOIPEPKQY	QRYFAETIQ	PQNYGPGIIRY	233
HTLV-I Pol	DLSSPTTLA HLQTIIDTDA FEOIPEPKQF	QRYFAETIQ	QQNYGPGIIRY	148
HIV SF2 Pol	HPAGLKKK-K SVTVLDVGD MFSVPLKKEF	RKYIAETIIS	INNETPGIIRY	299
Consensus	DLISPT.L. HLQTIIDTDA FEOIPEPKQF	QRYFAETIQ	.QNYGPGIIRY	300
HTLV-II Pol	AWIVLEQCFK NSPILTEQQLDAVENEMKRM	FETSTIVQYM	DEILLASPTN	283
HTLV-I Pol	AWKVLQCFK NSPILTEQQLAHILQPIRQA	FEOCTILOYM	DEILLASPSH	198
HIV SF2 Pol	QYNVLEQCFK GSEPIEGSSMUKKLEPFRKQ	NEDIVIMQYM	DELYVGSOLE	349
Consensus	AW.VLEQCFK NSEVLEE.Q...E.E.K. FE...T...QYMDEILLASP..			350
HTLV-II Pol	EELQQLSOLT QALTTHTGLP ISOKTQCTP	GQIRFGQVI	SPNHITVEST	333
HTLV-I Pol	EDLLLLSEAT VASLISHGLP VGENKTQCTP	GTIKFGQII	SPNHITVEST	248
HIV SF2 Pol	IGQHRTKIEE RQHLRLWGF TTPKKKQKE	PPFLWAGYEL	HPQKWIVQPI	399
Consensus	E.L..LS..T ..L..HGLP .S..KTQCTP	G.I.FGQ.I	SPNHITVEST	400
HTLV-II Pol	PTIRIKSQWLTLEOVILGE IQWMSKGTP	LRKHLSYS	ATHGYRDPRA	383
HTLV-I Pol	PTVIRSRWALPFLCALICE IQWMSKGTP	LRQPLHSLYC	ALQRTDPRD	298
HIV SF2 Pol	-MLEKDSWVNIQKLVCK LNPASQIYAG	IK--VKCK	LRGRTKALTE	446
Consensus	PT.IIKS..L.L.L.LICE IQWMSKGTP	LR..L.S.Y. AL.G..DPR.		450

Untitled-14 Formatted Alignment

HTLV-II Pol	CHITTPQQLH	ATHAICGATD	HNCRGRLNPA	LPLTGLISTD	TSGLTTSVIFQ	433
HTLV-I Pol	CHIMNPQVQ	SLVQLRQALS	QNCRSRLVQT	LPLTGAIMET	LTGLTITVVFQ	348
HIV SF2 Pol	VIELTEEAEL	ETLAENREILK	EPVHGVIYDP	SKDLVAETQ	KQCGQGWYQ	495
Consensus	.I.I.TP.Q..	.L...RQAL.	.NCRGRL...	LPLTG.I.L.	..GTT.V.FQ	500
HTLV-II Pol	PKQWFLAWL	HTPHPTSLC	PWGHLACTI	LTLPRMTLOH	YGQLCQSFHH	483
HTLV-I Pol	SKQWPLVWL	HAPLPHTSQ	PWGQLLASAV	LLLPRMTLOS	YGLLCQTIHH	398
HIV SF2 Pol	IYQE-LFKNL	KITGKYARMG	AHTNDVKQLT	EAVGRITLOS	IVIWGKIPKF	544
Consensus	.KQ.WEL.WL	HDP.P.TS.C	PWG.LLA...	L.LPRMTLOS	YG.LCQT.HH	550
HTLV-II Pol	NMSKQALC-D	FLRNSPHPSV	GILIHMGFR	HNLGSQPSGP	WKTLLHLPTL	532
HTLV-I Pol	NISTQTFN-Q	FIQTSDHPSV	HILLHSHRF	KNLGAQTGEL	WNITFLKTAAP	447
HIV SF2 Pol	KLPICKETWE	AWWTEYQOAT	WIPEWEFVNT	PHLVKLWYQL	EKDPIVGAET	594
Consensus	N.S.Q....-F	..TS.HPSV	.ILL.HH..RF	.NLG.Q...L	WKT.L.L.A..	600
HTLV-II Pol	LQEPRLLRPI	FTLSPVVLIT	APCLFSDGSP	QKAYVVLWDQ	TILQQDITPL	582
HTLV-I Pol	LAPVKALMPV	FTLSPVIINT	APCLFSDGST	SRAAYILWVK	QILSQRSFPL	497
HIV SF2 Pol	FYVDGAANRE	TKLGKAGYVT	DRGRQKVSL	TDITNQKTSL	QAIHLALQDS	644
Consensus	L....AL.P.	FTLSPV...T	APCLFSDGS.	...AAY.LWD.	QIL.Q...PL	650
HTLV-II Pol	PSHETHSAOK	GELLALICGL	RAAKPWPSLN	IFLDSKYLIK	YLHSLAIGAF	632
HTLV-I Pol	PPPH-KSAQR	AELLGLLHGL	SSARSWRCLN	IFLDSKYLH	YLRTIALGTF	546
HIV SF2 Pol	GLEVNIVIDS	QYALGIIQAQ	PKSESELVS	QIIEQLIKKE	KVYLAWWPAH	694
Consensus	P.....SAQ.	.ELLGLI.GL	..A..W..LN	IFLDSKYL..	YL..LA.GAF	700
HTLV-II Pol	IGTSAHQTLQ	AALPPLLQCK	TIYHHRSH	TNLPPPISTF	NEYTDSHILA	682
HTLV-I Pol	QGRSSQAPFO	ALLPRLLSRK	VVYLHHRSH	TNLPPPIISRL	NALTDAILLI	596
HIV SF2 Pol	KGIGGNEQVD	KLVSAGI-RK	VLFLDGL---	DKAQEEHEKY	HSNWRAM--A	738
Consensus	.G.S.....Q	ALLP.LL.RK	V.YLHHRSH	TNLPPPIIS..	N..TDAL..A	750
HTLV-II Pol	PLVHQLRQGL	HGLTHCNQRA	LVSFGATPRE	AKSLVQICHT	QOTINSQHHM	732
HTLV-I Pol	PVLQISEAEL	HSFTHCGQTA	LTLQGATTTE	ASNILRECHA	GRGGNPQHOM	646
HIV SF2 Pol	SDFNQLPE---	-----VV-----	-----	AKETVASCOK	QO--LKGEAM	765
Consensus	P...L.L..L	H..THC.Q.A	LV..GAT..E	AK.IV.SCH.	QO...N.QH.M	800
HTLV-II Pol	PRGYRRGILL	ENHIVGCEM	EFKYKRYKYC	LEVWVDTFSG	ASVSCKKKE	782
HTLV-I Pol	PRGHRRGILL	ENHIVGCEM	EFKYKNTLYR	LEVWVDTFSG	ASATQKRKE	696
HIV SF2 Pol	-HQAQDCS--	EG-TAQLDQ	MLEGKIILVA	VAV-ASGY--	-EEAEVIPAE	807
Consensus	PRG..RRGILL	ENHIVGCEM	..E.KYK..LY.	LEVWVDTFSG	ASVA..K.KK	850
HTLV-II Pol	ISCEHISAVL	QAISLLGKPL	HINIVGCPAF	ISQEFQEFCT	SYRIKSTHII	832
HTLV-I Pol	ISSEISSLIL	QAIAHLGKPS	YINIVGCPAY	ISQDFLNMCT	SLAIRATTHIV	746
HIV SF2 Pol	IGQDAYFID	KLGRWPVKT	-HIVGNSNF	TSITTVKAACW	WAGIKQEFGL	856
Consensus	IS.EIIS..L	QAI..LGKP.	..INIVGCPAF	.SQ.F...CT	S...IKH..THI	900

Untitled-14 Formatted Alignment

HTLV-II Pol	PYNHTSSGLVVERINGVIKNL	LNKYLDCPN	PLDNAIHKA	LWTLNQLNVM	882	
HTLV-I Pol	PYNHTSSGLVVERINGVIKNL	LYKYFTKPD	PMDNALSIA	LWTINHLNVL	796	
HIV SF2 Pol	PYNHTSSGLVVERINGVIKNI	IGQVRDQAEH	KTAVQMAVF	IHNFKRKGGI	906	
Consensus	PYNHTSSGLVVERINGVIKNI	L.KY...D.P.	P.DNA...A	LWT.N.LNV.	950	
HTLV-II Pol	NPSGKTRWQI	HHSPPLPPIP	EASTPPKPPP	KWFYKLPGL	TNQWKGFLQ	932
HTLV-I Pol	TNCHKTRWQL	HHSPRLQPIP	STRSLSNKQT	HWYYFKLPGL	NSRQWKGPE	846
HIV SF2 Pol	GGYSAGERIV	DIIATDIQTK	ELQKQITKIQ	NFRVY-YRDS	REPLWKGPAK	955
ConsensusKTRWQ.	HHSP.L.PIP	E.....K..	.W.YYKLPGLWKGP..	1000
HTLV-II Pol	STQEAAGAL	LSIEGS-PRW	TEWRFKKAA	CPRPDASELA	EHAATDHH	981
HTLV-I Pol	ATQEAAGAL	IPVSASSAQW	TEWRLIKRAA	CPRPVGGP-A	DPKEKDLOHH	895
HIV SF2 Pol	LLWKGECAVV	IQDNSD-IKV	MPRR--KAKI	IRDYGKQ MAG	DDCVASRODE	1002
Consensus	.TQEAAGAL	I....S-..W	TEWE.LK.AA	CPRP.....A	D....D.OHH	1050
HTLV-II Pol	G					982
HTLV-I Pol	G					896
HIV SF2 Pol	D					1003
Consensus	G					1051

Untitled-13 Formatted Alignment

HTLV-I/II
GAG ALIGNMENT

HTLV-II Gag	MGQIHGHSPT PTPKAPRGES THHWLNELQA AYRIEPEPSD FDRQOIRRET	50
HTLV-I gag	MGQIFSRAS PTPRHPRGIA AHHWLNELQA AYRIEPEPS YDRFOIKKET	50
Consensus	MGQH...S... PTP...PRGI... THHWLNELQA AYRIE...PS... DR...IR...ET	50
HTLV-II Gag	KIAIKTPHWL NPTIYSLIAS LIPKGYPCRV VETILNITAKN QVSPSAPAAP	100
HTLV-I gag	KIALETPARI QPNIYSLIAS LIPKGYPCRV NEILHITITQT Q-----AQ	93
Consensus	K...AL...TP... P...IYSLIAS...L...PKGYPCRV...ET...IT... Q.....A...	100
HTLV-II Gag	VETPICPTTT PEPPEPESP -----FAHV PPEVVEPTIT QCFEITLIFEC	143
HTLV-I gag	IESR----- PEPPEPESP HDPPDSEPOI PPEVVEPTAP QVLEFMEIFEC	137
Consensus	V...P...C...P...T...T... P...P...P...E...P...S...P... F...A...H...V... P...P...V...V...E...P...T...I...T... Q...C...F...E...I...T...L...I...F...E...C...	150
HTLV-II Gag	AFSAHWPWOM KDLOAIKQEV SSSALGSPQF MOTI RLAIVQQ FDEPAKDLQD	193
HTLV-I gag	APNHWPWOM KDLOAIKQEV SQALGSPQF MOTIRLAIVQQ FDEPAKDLQD	187
Consensus	AE...HRENDM...KDLOAIKQEV...S...A...L...GSPQF...MOT...RLAIVQQ...FDEPAKDLQD	200
HTLV-II Gag	LLOYLCSLV VSLHGOOLYT LITLDAETRCM IGVNEVAGPL RVOANNPAQQ	243
HTLV-I gag	LLOYLCSLV VSLHGOOLIS LITLDAETRCI IGVNEVAGPL RVOANNPAQQ	237
Consensus	LLOYLCSLV...VSLHGOOL...Y...T... L...I...T...L...D...A...E...T...R...C...M... I...G...V...N...E...V...A...G...P...L... R...V...O...A...N...N...P...A...Q...Q...	250
HTLV-II Gag	GLRREYQCLW LAEFAALPGN TRDPSWASIL QGLEEPPYCAF VERENVAHEN	293
HTLV-I gag	GLRREYQCLW LAEFAALPGS AKDPSWASIL QGLEEPPYCAF VERENVAHEN	287
Consensus	GLRREYQ...CLW...LAEFAAL...PG...N... TRDPSWASIL...QGLEEPPYCAF...VERENVAHEN	300
HTLV-II Gag	GLPEGTPEKP IERSLAYSNA NKECORLQA RCHTNSPLGE MLRIICQAWIE	343
HTLV-I gag	GLPEGTPEKP IERSLAYSNA NKECORLQA RCHTNSPLGD MLRIICQAWIE	337
Consensus	GLPEGTPEKP...IERSLAYSNA...NKECORLQA...RCHTNSPLGE...MLRIICQAWIE	350
HTLV-II Gag	KDKTKVLEWQ ERPEETOPC ERCKVGHWS RDCTOPRPPP GPCPLCODES	393
HTLV-I gag	KDKTKVLEWQ EKPPENOPC ERCKVGHWS RDCTOPRPPP GPCPLCODET	387
Consensus	KDKTKVLEWQ...E...R...P...E...E...T...O...P...C... ERCKVGHWS...RDCTOPRPPP...GPCPLCODE...	400
HTLV-II Gag	HWKRDCEPKK -----POEEG SHHMDIST GTTEENSL RGSII	433
HTLV-I gag	HWKRDCEPKK ETIPEPEEE SHHMDIST-- GDIPHEKFI GOEIV	429
Consensus	HWKRDCEPKK...E...T...I...P...E...P...E...E... SHHMDIST...GTTEENSL...RGSII	444

Untitled-13 Formatted Alignment

HTLV-I/II: HIV-I
GAG ALIGNMENT

HTLV-II Gag	MSQIHG-LSPTPIPKAPRGLSTHHWLNFLQAAAYRLQPRPSDFLEQQLRRF	49
HTLV-I gag	MSQIFS-RSA SPIPRPPRGLAAHHWLNFLQAAAYRLEPGPS SYDFHQLKKF	49
Hiv SF2 Gag	MGARASVLSG GELDKWEKIRLRPGGKKKYQ LKHIVWASRE LERFAINPGL	50
Consensus	MSQI.S-LS. .PIPK.PRGL ..HHWLNFLQAAAYRL.P.PS ..DEQL..F	50
HTLV-II Gag	EKLALKTPIW LNPIFYSLA SLIPKGYPGR VVEIINILVK NOVSPSAPAA	99
HTLV-I gag	EKLALETPAR ICPINYSLLA SLLPKGYPGR VNEILHILIQ TQ-----A	92
Hiv SF2 Gag	LETSEGCRQI LGQLQFSLKPGSEEIRSLYN TVATLYCVHQ KIEVKDTKEA	100
Consensus	EK.AL.TP.. L.PIYSLA SL.PKGYPGR VVEIL.IL.Q .Q.....A	100
HTLV-II Gag	FVPTPICPTT TPPPPPPSP -----EAH VHPYVEPTT TQCFPIHP	142
HTLV-I gag	QIPSR----- -PAPPPSP THDPDSDPQ IHPYVEPTA PQVLPVMHP	136
Hiv SF2 Gag	LDKIEEEQNK SKKKAQQTAA DTGNSSQVSO NYETIVQLQG QMVHQPISP	150
Consensus	..P..... .P.PPPP.SPQ.HPYVEPT. .QV.P..HE.	150
HTLV-II Gag	GAPSAHRPWMDL-QATKQ EVSSALG-S PQFMQILRLA MQQFDPTAKD	190
HTLV-I gag	GAPNHRPWMDL-QATKQ EVSQAAG-S PQFMQILRLA MQQFDPTAKD	184
Hiv SF2 Gag	TLNAWVKVVE EKAFSPENIP MFSALAECAI PQDNLIMLNI VGGHQAAMQM	200
Consensus	GAP..HRPWMDL-QATKQ EVS..A.G-S PQFMQILRLA MQQFDPTAKD	200
HTLV-II Gag	EQLLQYLCS SL--VVSLEH QQLN-TLITE AETRGMIGYN PMAGPLRMQA	237
HTLV-I gag	EQLLQYLCS SL--VASLEH QQLD-SLISE AETRGIIGYN PLAGPLRVQA	231
Hiv SF2 Gag	EKTINEEAA EWDRLHPVHA GPIAPGQMR PRGSDIAGTT STLQEQIGWM	250
Consensus	EQLLQYLCS SL--V.SLEH QQL.-.LI.E AETRGIIGYN P.AGPLR.QA	250
HTLV-II Gag	NPAQQGLRR EYQNLWLA AF STLPGNTRDP SWAATLOGLE EEPYCAFVERL	287
HTLV-I gag	NPAQQGLRR EYQQLWLA AF ALPGSAKDP SWASITLOGLE EEPYHAFVERL	281
Hiv SF2 Gag	TNNPIPVGE IYKRWIILGL NKIVRMYSP SILLIRQGP KEFRDYVIRF	300
Consensus	NNP.QQGLRR EYQ.LWLA AF .LPG...DP SWA.ITLOGLE EEPY.AFVERL	300
HTLV-II Gag	NVIEDNGLPE GTHKPIILRS TAYSANKEC OKILQARCHI NSHLEGEMIRA	337
HTLV-I gag	NVIEDNGLPE GTHKPIILRS TAYSANKEC OKILQARCHI NSHLEGEMIRA	331
Hiv SF2 Gag	YKIRREQAS QDVKNWMTED ILVQANPFC KTIKALCPA -ATLEEMMTA	349
Consensus	N.VIDNGLPE GTHKPIILRS TAYSANKEC OKILQARCHI NSHLEGEMIRA	350
HTLV-II Gag	CGAW-TIEKIK IKME-----VVQP ---RRPPPTQ FQTRCGKMGH	371
HTLV-I gag	CGIW-TIEKIK IKME-----VVQP ---KKPPPNQ FQTRCGKACH	365
Hiv SF2 Gag	CGVGGECHK ARVAEAMSQ VNSVTVMOK GNFKNQKTV KGRNCGKECH	399
Consensus	CG.W-TIEKIK IKME-----VVQP ---K.PPPTQ FQTRCGK.AH	400
HTLV-II Gag	WSREITQEP PPG-PC-----PE-CQEP-----SHA--KRDCI---Q	401
HTLV-I gag	WSREITQEP PPG-PC-----PE-CQEP-----THA--KRDCI---R	395
Hiv SF2 Gag	IAKNRAPRK KGCWKCGREG HOMKDIYERQ ANFLGKIAPS HKGRGNGFLQ	449
Consensus	WSREITQEP PPG-PC-----PE-CQEP-----HA--KRDCI---Q	450

Untitled-13 Formatted Alignment

HTLV-II Gag	LK E --- E QE E ---GE--- -PLLL E ST SG---TTEEK N SLR E I---	433
HTLV-I gag	LK E TI E PE E P E --- E --- E --- -ALL E LE--- AD---IPHPK N FIG E V---	429
Hiv SF2 Gag	NR E PT A PP A E SFGFG E TT TP P Q K E P I D KGLYPL T SLR S LF G N D PSS Q	499
Consensus	L K E ... E ,. E ---GE--- -PLLL EG---.T..K N ..G E ..---	500